

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/911,423DATE: 03/25/98
TIME: 16:43:00

INPUT SET: S24403.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED
04-16-98

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert

(ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
REAGENTS

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: DNAX Research Institute
(B) STREET: 901 California Avenue
(C) CITY: Palo Alto
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94304-1104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,423
(B) FILING DATE: 14-AUG-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/023,419
(B) FILING DATE: 16-AUG-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/027,901
(B) FILING DATE: 07-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Ching, Edwin P.
(B) REGISTRATION NUMBER: 34,090
(C) REFERENCE/DOCKET NUMBER: DX0612K

(ix) TELECOMMUNICATION INFORMATION:

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47 (A) TELEPHONE: 650-852-9196
48 (B) TELEFAX: 650-496-1200
49
50

51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 1073 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58

59 (ii) MOLECULE TYPE: cDNA
60

61
62 (ix) FEATURE:
63 (A) NAME/KEY: CDS
64 (B) LOCATION: 68..751
65
66

67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68

69	CTCGAGATCC ATTGTGCTGG AAAGGGAACCT CCTGAAATCA GCCGACAGAA GACTCAGGAG	60
70		
71	AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT	109
72	Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys	
73	1 5 10	
74		
75	GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC	157
76	Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly	
77	15 20 25 30	
78		
79	CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC	205
80	Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser	
81	35 40 45	
82		
83	CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT	253
84	Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys	
85	50 55 60	
86		
87	GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG	301
88	Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys	
89	65 70 75	
90		
91	CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGC GAT ATT	349
92	His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile	
93	80 85 90	
94		
95	GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA	397
96	Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala	
97	95 100 105 110	
98		
99	GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA	445

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100 Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
101                               115                               120                               125
102
103 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC      493
104 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
105                               130                               135                               140
106
107 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC      541
108 Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
109                               145                               150                               155
110
111 CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC      589
112 Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
113                               160                               165                               170
114
115 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC      637
116 Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
117                               175                               180                               185                               190
118
119 CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC      685
120 Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
121                               195                               200                               205
122
123 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT      733
124 Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
125                               210                               215                               220
126
127 CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC      781
128 Leu Gly Gly Arg Trp Pro
129                               225
130
131 CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC      841
132
133 CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG      901
134
135 TGAGTTACGA TTGGGCCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT      961
136
137 CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG      1021
138
139 TTTAGTAACC TGAAAAAAAAA AAAAAAAGG GCGGCCGCGG AGGCCGAATT CC      1073
140
141
142 (2) INFORMATION FOR SEQ ID NO:2:
143
144 (i) SEQUENCE CHARACTERISTICS:
145 (A) LENGTH: 228 amino acids
146 (B) TYPE: amino acid
147 (D) TOPOLOGY: linear
148
149 (ii) MOLECULE TYPE: protein
150
151 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
152
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153 Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
154   1                      5                      10                      15
155
156 Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
157          20                      25                      30
158
159 Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
160          35                      40                      45
161
162 Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
163          50                      55                      60
164
165 Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
166          65                      70                      75                      80
167
168 Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
169          85                      90                      95
170
171 Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
172          100                      105                      110
173
174 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
175          115                      120                      125
176
177 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
178          130                      135                      140
179
180 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
181          145                      150                      155                      160
182
183 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
184          165                      170                      175
185
186 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
187          180                      185                      190
188
189 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
190          195                      200                      205
191
192 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
193          210                      215                      220
194
195 Gly Arg Trp Pro
196 225

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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206      (ii) MOLECULE TYPE: cDNA
207
208
209      (ix) FEATURE:
210          (A) NAME/KEY: CDS
211          (B) LOCATION: 1..723
212
213
214      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
215
216      ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG      48
217      Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
218          1              5              10              15
219
220      GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC      96
221      Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
222          20              25              30
223
224      GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC      144
225      Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
226          35              40              45
227
228      TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG      192
229      Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
230          50              55              60
231
232      GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC      240
233      Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
234          65              70              75              80
235
236      TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA      288
237      Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
238          85              90              95
239
240      GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT      336
241      Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
242          100              105              110
243
244      ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC      384
245      Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
246          115              120              125
247
248      AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT      432
249      Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
250          130              135              140
251
252      GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA      480
253      Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
254          145              150              155              160
255
256      GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC      528
257      Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
258          165              170              175

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SEQUENCE VERIFICATION REPORT
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Original Text